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EXAMINER

SMITH, CAROLYN L

ART UNIT

PAPER NUMBER

1631

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Please find below and/or attached an Office communication concerning this application or proceeding.

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DETAILED ACTION

A request for continued examination under 37 CFR 1.114, including the fee set forth in 37 CFR 1.17(e), was filed in this application after final rejection. Since this application is eligible for continued examination under 37 CFR 1.114, and the fee set forth in 37 CFR 1.17(e) has been timely paid, the finality of the previous Office action has been withdrawn pursuant to 37 CFR 1.114. Applicants' submission, filed 7/5/05, has been entered.

Amended claims 1, 5, 9, 51, and 59, filed 7/5/05, are acknowledged.

Claims herein under examination are 1, 5, 9, 51, and 59.

Claim Rejections – 35 USC § 103

The following is a quotation of 35 U.S.C. 103(a) which forms the basis for all obviousness rejections set forth in this Office action:

(a) A patent may not be obtained though the invention is not identically disclosed or described as set forth in section 102 of this title, if the differences between the subject matter sought to be patented and the prior art are such that the subject matter as a whole would have been obvious at the time the invention was made to a person having ordinary skill in the art to which said subject matter pertains. Patentability shall not be negated by the manner in which the invention was made.

This application currently names joint inventors. In considering patentability of the claims under 35 U.S.C. 103(a), the examiner presumes the subject matter of the various claims was commonly owned at the time any inventions covered therein were made absent any evidence to the contrary. Applicant is advised of the obligation under 37 CFR 1.56 to point the inventor and invention dates of each claim that was not commonly owned at the time a later invention was

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made in order for the examiner to consider the applicability of 35 U.S.C. 103(c) and potential 35 U.S.C. (e), (f) or (g) prior art under 35 U.S.C. 103(a).

Claims 1, 5, 9, 51, and 59 are rejected under 35 U.S.C. 103(a) as being unpatentable over Cummings et al. (Genomics, Vol. 6, No. 5, Sept-Oct 2000, pages 513-525) in view of Exley et al. (US 2002/0164331 A1).

Cummings et al. describe methods of using host gene microarrays to explore gene level expressions that follow infection of a microbial pathogen (abstract). Cummings et al. describe host profiling as a way to identify gene expression signatures unique for each pathogen to be used as a tool for diagnosis, prognosis, and clinical management of infectious disease (abstract). The instant specification states a “stimulus” includes bacteria, fungi, viruses, or components thereof (page 5, first paragraph). On page 15, lines 20-22, the instant specification refers to “stimulus-specific” and “pathogen-specific” genes as genes that are “specifically-regulated by a pathogen, pathogen-class or component thereof”. Therefore, the unique gene expression signature due to pathogen infection mentioned by Cummings et al. encompasses “pathogen-specific” genes as stated in claim 1. Cummings et al. describe that gene expression profiling of host-pathogen interactions are emerging in the science field (page 514, col. 1, first paragraph). Cummings et al. describe measuring relative gene expression, noting relative excess, and analyzing experiments with red (positive values indicating relative excess of red or increased expression) and green (negative values indicating relative excess of green or decreased expression) and black (near zero values or no expression) (Figure 1 caption), using standard, robust statistical methods to assign significance values to gene expression measurements (page 516, col. 1, third paragraph), and observing fourfold differences and substantial changes in

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expression experiments (page 520, col. 2, first two paragraphs) which represents statistically significant increase or decrease in expression. Cummings et al. describe examining infected cultured cells (page 520, col. 1, fifth paragraph) which represents cells that have come into contact with a pathogen. Cummings et al. describe preparing and purifying mRNA from eukaryotic cells (including humans, a type of mammal) to be used in hybridization experiments with microarrays (Figure 1; page 514, col. 2, second paragraph; and page 515, col. 1, first paragraph and col. 2, second paragraph). Cummings et al. describe isolating and labeling RNA from microbial samples as well (page 518, col.2, third paragraph). Cummings et al. describe labeling mRNA in the microarray methodology (page 515, col. 1, first paragraph). Cummings et al. describe performing a cross-species comparison of many different pathogens (page 517, col. 1, second paragraph) which represent reference gene expression profiles (as the instant claims do not mention that the reference gene profile is from the same organism), as stated in instant claims 1, 5, 9, 51, and 59. Cummings et al. describe monitoring gene expression in *M. tuberculosis*, a pathogen, while it infects cultured monocytes (page 518, col. 1, second paragraph). Cummings et al. describe genes that are specifically expressed during infection (page 518, col.2, third paragraph). Cummings et al. describe comparing arrays to monitor gene expression in primary human fibroblasts infected (infected human) with human CMV in reference to uninfected cells (control) and noting fourfold differences between infected and uninfected human genes (page 520, col. 2, first paragraph) which represents an increased or decreased expression of at least one pathogen-specific gene relative to expression of the pathogen-specific gene in a reference (uninfected control) gene expression profile, as stated in all instant claims. Cummings et al. describe examining HIV-1 infection in CD4-positive T cells and noting differential expression in

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20 human genes (page 520, col. 2, second paragraph). Cummings et al. describe examining response to host cells to infection with bacterial pathogens (page 520, col. 2, third paragraph). Cummings et al. describe comparison of gene expression profiling data from human monocytes infected by different strains of virus (page 521, col. 1, third paragraph) which is interpreted to be an analysis of gene profiles relative to other reference profiles to identify specific genes for a particular pathogen. Cummings et al. describe microarrays used in measuring responses of cultured cells to distinct external stimuli (page 521, col. 2, second paragraph). Cummings et al. describe measuring gene expression in leukocytes to find signatures diagnostic of infection by specific pathogens (page 521, col. 2, third paragraph). Cummings et al. describe using these host gene expression signatures as diagnostic markers (or probes) of infection (page 521, col. 2, fourth paragraph). Cummings et al. describe identification of gene expression profiles common to many different pathogens (page 522, col. 1, second paragraph). Cummings et al. do not specifically describe antigen presenting dendritic or immature antigen presenting dendritic cells (claims 1, 5, 9, 51, and 59).

Exley et al. describe T cells that are lymphocytes that participate in multiple cell-mediated immune reactions, such as recognition and destruction of infected or cancerous cells (paragraph 0004). Exley et al. describe diagnostic methods involving T cells (abstract). It is noted that Applicants supplied an online Medical dictionary definition of dendritic cell that includes a T lymphocyte. Exley et al. describe using immature and mature dendritic cells in various experiments, including DNA microarrays (paragraphs 0117, 0220, 0224, 0245, 0249, 0251) and describe contacting T cells with an antigen or antigen presenting cells wherein the antigen is an infectious pathogen (paragraphs 0043 and 0126) which represents antigen

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presenting dendritic cells and immature antigen presenting dendritic cells. Exley et al. describe identifying gene expression patterns using DNA microarrays and determining expression profiles with a control (reference) (paragraphs 0217, 0219, and 0220). Exley et al. describe isolating and labeling RNA from the T cells that were then hybridized on DNA microarray chips (paragraph 0229). Exley et al. describe genes that are differentially expressed (paragraph 0113 and Figure 25A) followed by determining and comparing changes in gene expression of specific genes identified in Figure 25A (paragraph 0114 and Figures 26A and B).

Cummings et al. state the interaction between a microbial pathogen and a host is the underlying basis of infectious disease (page 513, col. 1, first paragraph). Cummings et al. also state that understanding the details of this interaction will help us identify virulence-associated microbial genes and host defense strategies and their regulated (page 513, col. 1, first paragraph). Cummings et al. state this information will guide the design of a new generation of medical tools (page 513, col. 1, first paragraph). Cummings et al. state explaining life at a molecular level is slow because gene function understanding lags behind and that high throughput methods are required (page 513, col. 1, second paragraph to col. 2, first paragraph). Cummings et al. state microarray-based approaches hold exceptional promise and will make substantial contributions for studying infectious disease (page 513, col. 2, third paragraph). Cummings et al. state the goals of functional genomics and microarray technology in infectious diseases will require additional technology, extensive data collection, and sophisticated computational tools (col. 522, col. 1, fourth paragraph). Exley et al. state there is a need to specifically monitor T cells in mammals for infections (paragraph 0014). As Cummings et al. state the goals of identifying and diagnosing host-pathogen interactions (page 522, col. 1, fourth paragraph), one of ordinary skill

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in the art would have been motivated to perform such microarray technology on cells, genes, and pathogens already known to be specific for a particular pathogen (abstract). Therefore, it would have been obvious to one having ordinary skill in the art at the time the invention was made to use the dendritic cells, such as those noted by Exley et al., in the microarray technology suggested by Cummings et al. in order to help further identify genes unique for each pathogen. One would have a reasonable expectation of success since T cells are already known to play a role in recognizing infected cells (Exley et al., paragraph 0004).

Thus, Cummings et al., in view of Exley et al. make obvious the instant invention.

Applicants argue that neither Cummings et al. nor Exley et al. disclose the claimed invention. This statement is found unpersuasive as these two references combined teach all of the limitations of the instant invention, as described above. Applicants summarize Exley et al. and again argue that T cells are not dendritic cells. This statement was previously found to be unpersuasive as the definition previously supplied by Applicants is overly broad. It is reiterated that no clear and concise definition of the phrase “dendritic cell” was stated in the specification. This lack of clear and concise definition has resulted in this phrase being broadly and reasonably interpreted, as stated in the rejection above. Applicants argue that nothing in Exley et al. disclose monitoring antigen presenting dendritic cells with regard to infection. This statement is found unpersuasive as the instant claims do not recite any “monitoring” step. Furthermore, Cummings et al. and Exley et al. describe every limitation in the instant invention, as noted above. Applicants are reminded that a single reference need not teach all the instantly claimed limitations by itself in a 35 USC 103 rejection, which is why this is a 35 USC 103 rejection as

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opposed to a 35 USC 102 rejection. Applicants argue that there would be no motivation to combine the Cummings et al. and Exley et al. references. This statement is found unpersuasive as Cummings et al. state an inefficiency between gene function understanding and high throughput methods as well as the promise of microarray-based technologies for studying infectious diseases. Exley et al. state there is a need to monitor T cells in mammals for infections. Therefore, both groups of authors provide adequate motivation to combine the references, because inefficiencies and needs are valid motivational reasons for combining technologies. Applicants again argue that Exley et al. do not teach the identification of pathogen-specific genes from T cells or antigen presenting dendritic cells. This statement is again found unpersuasive as Cummings et al. and Exley et al. describe every limitation in the instant invention, as already discussed above. Applicants' arguments are deemed unpersuasive for the reasons given above.

Conclusion

No claim is allowed.

Papers related to this application may be submitted to Technical Center 1600 by facsimile transmission. Papers should be faxed to Technical Center 1600 via the PTO Fax Center. The faxing of such papers must conform to the notices published in the Official Gazette, 1096 OG 30 (November 15, 1988), 1156 OG 61 (November 16, 1993), and 1157 OG 94 (December 28, 1993) (See 37 CFR §1.6(d)). The Central Fax Center number for official correspondence is (571) 273-8300.

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Any inquiry concerning this communication or earlier communications from the examiner should be directed to Carolyn Smith, whose telephone number is (571) 272-0721. The examiner can normally be reached Monday through Thursday from 8 A.M. to 6:30 P.M.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Andrew Wang, can be reached on (571) 272-0811.

Any inquiry of a general nature or relating to the status of this application should be directed to Legal Instruments Examiner Yolanda Chadwick whose telephone number is (571) 272-0514.

August 15, 2006

A handwritten signature in black ink, appearing to read 'Carolyn Smith', with a stylized flourish at the end.

Carolyn Smith
Examiner
AU 1631